

SEQ ID NO	Description	Sequence
1	Nucleic acid sequence encoding the full-length Q144 allotypic variant of human TSG-6.	cagtcacatt tcagccactg ctctgagaat ttgtgagcag cccctaacag gctgttactt 60 cactacaact gacgat atg atc atc tta att tac tta ttt ctc ttg cta tgg 112 Met Ile Ile Leu Ile Tyr Leu Phe Leu Leu Leu Trp 1 5 10 gaa gac act caa gga tgg gga ttc aag gat gga att ttt cat aac tcc 160 Glu Asp Thr Gln Gly Trp Gly Phe Lys Asp Gly Ile Phe His Asn Ser 15 20 25 ata tgg ctt gaa cga gca gcc ggt gtg tac cac aga gaa gca cgg tct 208 Ile Trp Leu Glu Arg Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ser 30 35 40 ggc aaa tac aag ctc acc tac gca gaa gct aag gcg gtg tgt gaa ttt 256 Gly Lys Tyr Lys Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe 45 50 55 60 gaa ggc ggc cat ctc gca act tac aag cag cta gag gca gcc aga aaa 304 Glu Gly Gly His Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys 65 70 75 att gga ttt cat gtc tgt gct gct gga tgg atg gct aag ggc aga gtt 352 Ile Gly Phe His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val 80 85 90 gga tac ccc att gtg aag cca ggg ccc aac tgt gga ttt gga aaa act 400 Gly Tyr Pro Ile Val Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr 95 100 105 ggc att att gat tat gga atc cgt ctc aat agg agt gaa aga tgg gat 448 Gly Ile Ile Asp Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp 110 115 120 gcc tat tgc tac aac cca cac gca aag gag tgt ggt ggc gtc ttt aca 496 Ala Tyr Cys Tyr Asn Pro His Ala Lys Glu Cys Gly Gly Val Phe Thr 125 130 135 140 gat cca aag caa att ttt aaa tct cca ggc ttc cca aat gag tac gaa 544 Asp Pro Lys Gln Ile Phe Lys Ser Pro Gly Phe Pro Asn Glu Tyr Glu 145 150 155 gat aac caa atc tgc tac tgg cac att aga ctc aag tat ggt cag cgt 592 Asp Asn Gln Ile Cys Tyr Trp His Ile Arg Leu Lys Tyr Gly Gln Arg 160 165 170 att cac ctg agt ttt tta gat ttt gac ctt gaa gat gac cca ggt tgc 640 Ile His Leu Ser Phe Leu Asp Phe Asp Leu Glu Asp Asp Pro Gly Cys 175 180 185 ttg gct gat tat gtt gaa ata tat gac agt tac gat gat gtc cat ggc 688 Leu Ala Asp Tyr Val Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly 190 195 200 ttt gtg gga aga tac tgt gga gat gag ctt cca gat gac atc atc agt 736 Phe Val Gly Arg Tyr Cys Gly Asp Glu Leu Pro Asp Asp Ile Ile Ser 205 210 215 220 aca gga aat gtc atg acc ttg aag ttt cta agt gat gct tca gtg aca 784 Thr Gly Asn Val Met Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr 225 230 235 gct gga ggt ttc caa atc aaa tat gtt gca atg gat cct gta tcc aaa 832 Ala Gly Gly Phe Gln Ile Lys Tyr Val Ala Met Asp Pro Val Ser Lys 240 245 250 tcc agt caa gga aaa aat aca agt act act tct act gga aat aaa aac 880 Ser Ser Gln Gly Lys Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn 255 260 265

		ttt tta gct gga aga ttt agc cac tta taa aaaaaaaaaa aaggatgac 930 Phe Leu Ala Gly Arg Phe Ser His Leu 270 275 aaaacacaca gtgtttatgt tggaatcttt tggaactcct ttgatctcac tgttattatt 990 aacatttatt tattattttt ctaaatgtga aagcaatata taatttaggg aaaattggaa 1050 aatataggaa actttaaacg agaaaatgaa acctctcata atcccactgc atagaataaa 1110 caagcgtaa cattttcata tttttttctt tcagtcattt ttctatttgt ggtatatgta 1170 tatatgtacc tatatgtatt tgcatttgaa attttggaa cctgctctat gtacagtttt 1230 gtattatact ttttaaatct tgaactttat aaacattttc tgaatcatt gattattcta 1290 caaaaacatg attttaaca gctgtaaaat attctatgat atgaatgttt tatgcattat 1350 ttaagcctgt ctctatttgt ggaatttcag gtcattttca taaatattgt tgcaataaat 1410 atccttgaac acaaaaaaaaa aaaaaaaaaa 1440
2	Amino acid sequence of full-length Q144 allotypic variant of human TSG-6. This allotypic variant has a glutamine residue (Q) at position 144. It is the most common allotypic variant and is found in approximately 86% of the Caucasian population (Nentwich et al. (2002) 277, 15354-15362).	Met Ile Ile Leu Ile Tyr Leu Phe Leu Leu Trp Glu Asp Thr Gln 1 5 10 15 Gly Trp Gly Phe Lys Asp Gly Ile Phe His Asn Ser Ile Trp Leu Glu 20 25 30 Arg Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ser Gly Lys Tyr Lys 35 40 45 Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe Glu Gly Gly His 50 55 60 Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly Phe His 65 70 75 80 Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly Tyr Pro Ile 85 90 95 Val Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile Ile Asp 100 105 110 Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr Cys Tyr 115 120 125 Asn Pro His Ala Lys Glu Cys Gly Gly Val Phe Thr Asp Pro Lys Gln 130 135 140 Ile Phe Lys Ser Pro Gly Phe Pro Asn Glu Tyr Glu Asp Asn Gln Ile 145 150 155 160 Cys Tyr Trp His Ile Arg Leu Lys Tyr Gly Gln Arg Ile His Leu Ser 165 170 175 Phe Leu Asp Phe Asp Leu Glu Asp Asp Pro Gly Cys Leu Ala Asp Tyr 180 185 190 Val Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly Phe Val Gly Arg 195 200 205 Tyr Cys Gly Asp Glu Leu Pro Asp Asp Ile Ile Ser Thr Gly Asn Val 210 215 220 Met Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr Ala Gly Gly Phe 225 230 235 240 Gln Ile Lys Tyr Val Ala Met Asp Pro Val Ser Lys Ser Ser Gln Gly 245 250 255 Lys Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn Phe Leu Ala Gly 260 265 270 Arg Phe Ser His Leu 275

3	The amino acid sequence of the Q144 allotypic variant of human TSG-6 without the signal sequence (corresponds to residues 18-277 of SEQ ID NO: 2).	Trp Gly Phe Lys Asp Gly Ile Phe His Asn Ser Ile Trp Leu Glu Arg 1 5 10 15 Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ser Gly Lys Tyr Lys Leu 20 25 30 Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe Glu Gly Gly His Leu 35 40 45 Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly Phe His Val 50 55 60 Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly Tyr Pro Ile Val 65 70 75 80 Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile Ile Asp Tyr 85 90 95 Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr Cys Tyr Asn 100 105 110 Pro His Ala Lys Glu Cys Gly Gly Val Phe Thr Asp Pro Lys Gln Ile 115 120 125 Phe Lys Ser Pro Gly Phe Pro Asn Glu Tyr Glu Asp Asn Gln Ile Cys 130 135 140 Tyr Trp His Ile Arg Leu Lys Tyr Gly Gln Arg Ile His Leu Ser Phe 145 150 155 160 Leu Asp Phe Asp Leu Glu Asp Asp Pro Gly Cys Leu Ala Asp Tyr Val 165 170 175 Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly Phe Val Gly Arg Tyr 180 185 190 Cys Gly Asp Glu Leu Pro Asp Asp Ile Ile Ser Thr Gly Asn Val Met 195 200 205 Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr Ala Gly Gly Phe Gln 210 215 220 Ile Lys Tyr Val Ala Met Asp Pro Val Ser Lys Ser Ser Gln Gly Lys 225 230 235 240 Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn Phe Leu Ala Gly Arg 245 250 255 Phe Ser His Leu 260
4	The nucleic acid sequence encoding the full-length R144 allotypic variant of human TSG-6.	cagtcacatt tcagccaactg ctctgagaat ttgtgagcag cccctaacag gctgttactt 60 cactacaact gacgat atg atc atc tta att tac tta ttt ctc ttg cta tgg 112 Met Ile Ile Leu Ile Tyr Leu Phe Leu Leu Leu Trp 10 gaa gac act caa gga tgg gga ttc aag gat gga att ttt cat aac tcc 160 Glu Asp Thr Gln Gly Trp Gly Phe Lys Asp Gly Ile Phe His Asn Ser 25 ata tgg ctt gaa cga gca gcc ggt gtg tac cac aga gaa gca cgg tct 208 Ile Trp Leu Glu Arg Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ser 30 35 40 ggc aaa tac aag ctc acc tac gca gaa gct aag gcg gtg tgt gaa ttt 256 Gly Lys Tyr Lys Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe 45 50 55 60 gaa ggc ggc cat ctc gca act tac aag cag cta gag gca gcc aga aaa 304 Glu Gly Gly His Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys 65 70 75 att gga ttt cat gtc tgt gct gct gga tgg atg gct aag ggc aga gtt 352 Ile Gly Phe His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val

		80 85 90 gga tac ccc att gtg aag cca ggg ccc aac tgt gga ttt gga aaa act 400 Gly Tyr Pro Ile Val Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr 95 100 105 ggc att att gat tat gga atc cgt ctc aat agg agt gaa aga tgg gat 448 Gly Ile Ile Asp Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp 110 115 120 gcc tat tgc tac aac cca cac gca aag gag tgt ggt ggc gtc ttt aca 496 Ala Tyr Cys Tyr Asn Pro His Ala Lys Glu Cys Gly Gly Val Phe Thr 125 130 135 140 gat cca aag cgg att ttt aaa tct cca ggc ttc cca aat gag tac gaa 544 Asp Pro Lys Arg Ile Phe Lys Ser Pro Gly Phe Pro Asn Glu Tyr Glu 145 150 155 gat aac caa atc tgc tac tgg cac att aga ctc aag tat ggt cag cgt 592 Asp Asn Gln Ile Cys Tyr Trp His Ile Arg Leu Lys Tyr Gly Gln Arg 160 165 170 att cac ctg agt ttt tta gat ttt gac ctt gaa gat gac cca ggt tgc 640 Ile His Leu Ser Phe Leu Asp Phe Asp Leu Glu Asp Asp Pro Gly Cys 175 180 185 ttg gct gat tat gtt gaa ata tat gac agt tac gat gat gtc cat ggc 688 Leu Ala Asp Tyr Val Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly 190 195 200 ttt gtg gga aga tac tgt gga gat gag ctt cca gat gac atc atc agt 736 Phe Val Gly Arg Tyr Cys Gly Asp Glu Leu Pro Asp Asp Ile Ile Ser 205 210 215 220 aca gga aat gtc atg acc ttg aag ttt cta agt gat gct tca gtg aca 784 Thr Gly Asn Val Met Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr 225 230 235 gct gga ggt ttc caa atc aaa tat gtt gca atg gat cct gta tcc aaa 832 Ala Gly Gly Phe Gln Ile Lys Tyr Val Ala Met Asp Pro Val Ser Lys 240 245 250 tcc agt caa gga aaa aat aca agt act act tct act gga aat aaa aac 880 Ser Ser Gln Gly Lys Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn 255 260 265 ttt tta gct gga aga ttt agc cac tta taa aaaaaaaaaaaggatgatc 930 Phe Leu Ala Gly Arg Phe Ser His Leu 270 275 aaaacacaca gtgtttatgt tggaatcttt tggaactcct ttgatctcac tgttattatt 990 aacattttatt tattattttt ctaaatgtga aagcaataca taatttaggg aaaattggaa 1050 aatataggaa actttaaacg agaaaatgaa acctctcata atccactgc atagaaataa 1110 caagcgtaa cattttcata tttttttctt tcagtcattt ttctatttgt ggtatatgta 1170 tatatgtacc tatatgtatt tgcatttgaa attttggaat cctgctctat gtacagtttt 1230 gtattatact ttttaaatct tgaactttat aaacattttc tgaaatcatt gattatttcta 1290 caaaaacatg attttaaca gctgtaaaat attctatgat atgaatgttt tatgcattat 1350 ttaagcctgt ctctattgtt ggaatttcag gtcattttca taaatattgt tgcaataaat 1410 atccttgaac aaaaaaaaaa aaaaaaaaaa 1440
5	The amino acid sequence of full-length R144 allotypic variant of human TSG-6. This allotypic	Met Ile Ile Leu Ile Tyr Leu Phe Leu Leu Leu Trp Glu Asp Thr Gln 15 1 5 10 Gly Trp Gly Phe Lys Asp Gly Ile Phe His Asn Ser Ile Trp Leu Glu 30 20 25 30 Arg Ala Ala Gly Val Tyr His Arg Glu Ala Arg Ser Gly Lys Tyr Lys

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		145 150 155 160 Leu Asp Phe Asp Leu Glu Asp Asp Pro Gly Cys Leu Ala Asp Tyr Val 165 170 175 Glu Ile Tyr Asp Ser Tyr Asp Asp Val His Gly Phe Val Gly Arg Tyr 180 185 190 Cys Gly Asp Glu Leu Pro Asp Asp Ile Ile Ser Thr Gly Asn Val Met 195 200 205 Thr Leu Lys Phe Leu Ser Asp Ala Ser Val Thr Ala Gly Gly Phe Gln 210 215 220 Ile Lys Tyr Val Ala Met Asp Pro Val Ser Lys Ser Ser Gln Gly Lys 225 230 235 240 Asn Thr Ser Thr Thr Ser Thr Gly Asn Lys Asn Phe Leu Ala Gly Arg 245 250 255 Phe Ser His Leu 260
7	The amino acid sequence of the Link module of human TSG-6 (corresponds to residues 37-128 of SEQ ID NOS: 2 and 5).	Val Tyr His Arg Glu Ala Arg Ser Gly Lys Tyr Lys Leu Thr Tyr Ala 1 5 10 15 Glu Ala Lys Ala Val Cys Glu Phe Glu Gly Gly His Leu Ala Thr Tyr 20 25 30 Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly Phe His Val Cys Ala Ala 35 40 45 Gly Trp Met Ala Lys Gly Arg Val Gly Tyr Pro Ile Val Lys Pro Gly 50 55 60 Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile Ile Asp Tyr Gly Ile Arg 65 70 75 80 Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr Cys Tyr 85 90
8	Nucleic acid sequence encoding Link_TSG6 used in the Examples (Day <i>et al.</i> (1996) <i>Protein Expr. Pruif.</i> 8, 1-16).	aggagatata cat atg ggt gtg tac cac cgt gaa gca cgg tct ggc aaa 49 Met Gly Val Tyr His Arg Glu Ala Arg Ser Gly Lys 1 5 10 tac aag ctc acc tac gca gaa gct aag gcg gtg tgt gaa ttt gaa ggc 97 Tyr Lys Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe Glu Gly 15 20 25 ggc cat ctc gca act tac aag cag cta gag gca gcc cgt aaa att gga 145 Gly His Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly 30 35 40 ttt cat gtc tgt gct gct gga tgg atg gct aag ggc cgt gtt gga tac 193 Phe His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly Tyr 45 50 55 60 ccc att gtg aag cca ggg ccc aac tgt gga ttt gga aaa act ggc att 241 Pro Ile Val Lys Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile 65 70 75 att gat tat gga atc cgt ctc aat agg agt gaa cgt tgg gat gcc tat 289 Ile Asp Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr 80 85 90 tgc tac aac cca cac gca aag taa gaattc 319 Cys Tyr Asn Pro His Ala Lys 95
9	The amino acid sequence of Link_TSG6 used in the Examples.	Gly Val Tyr His Arg Glu Ala Arg Ser Gly Lys Tyr Lys Leu Thr Tyr Ala Glu Ala Lys Ala Val Cys Glu Phe Glu Gly Gly His Leu Ala Thr Tyr Lys Gln Leu Glu Ala Ala Arg Lys Ile Gly Phe His Val Cys Ala Ala Gly Trp Met Ala Lys Gly Arg Val Gly Tyr Pro Ile Val Lys

	Residues 2-93 of SEQ ID NO: 9 correspond to SEQ ID NO: 7 (residues 37-128 of SEQ ID NOs: 2 and 5).	Pro Gly Pro Asn Cys Gly Phe Gly Lys Thr Gly Ile Ile Asp Tyr Gly Ile Arg Leu Asn Arg Ser Glu Arg Trp Asp Ala Tyr Cys Tyr Asn Pro His Ala Lys
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Figure 1

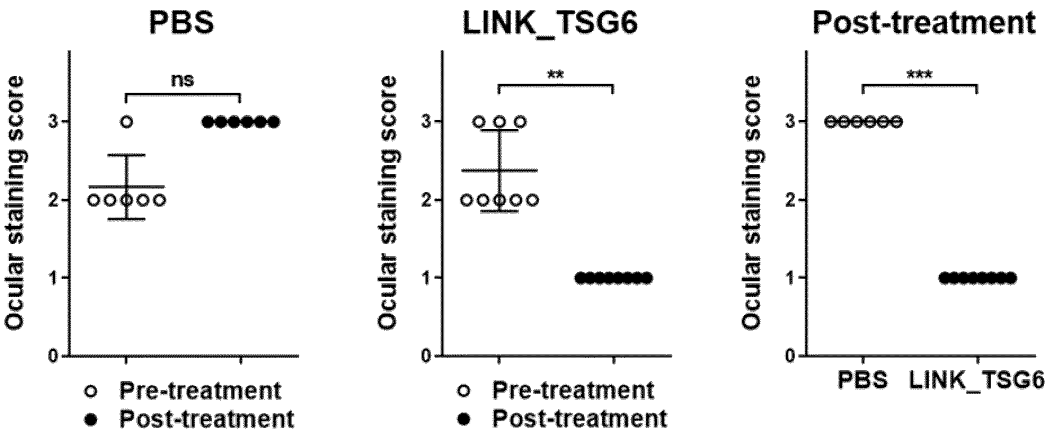


Figure 2A

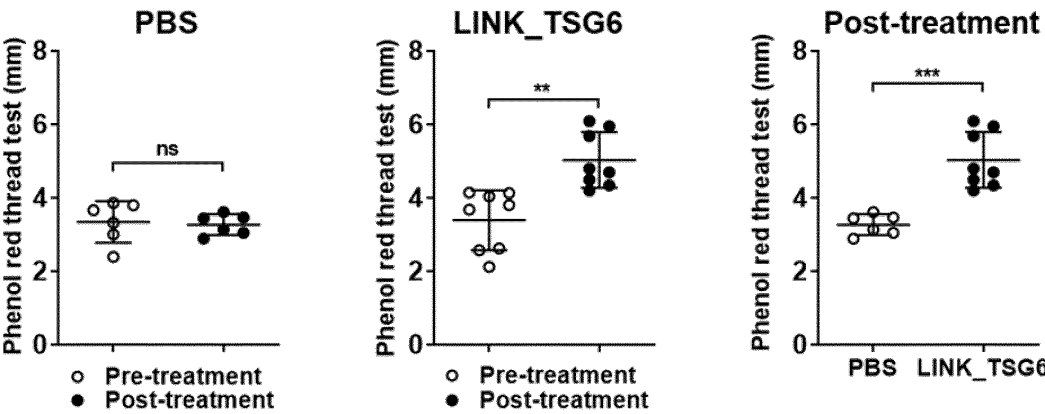


Figure 2B

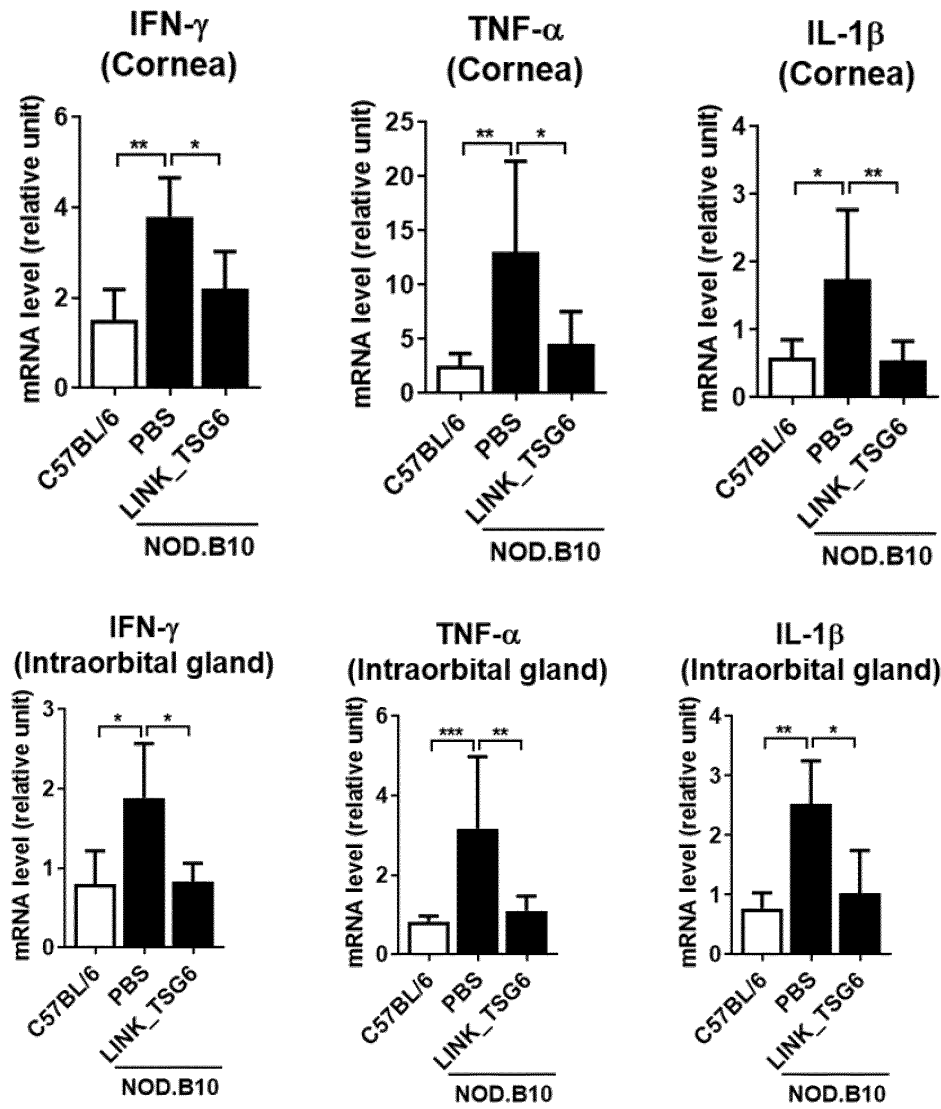
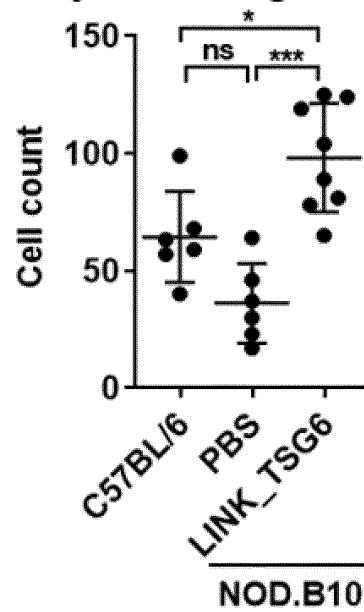


Figure 2C

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Conjunctival goblet cell**Figure 2D**

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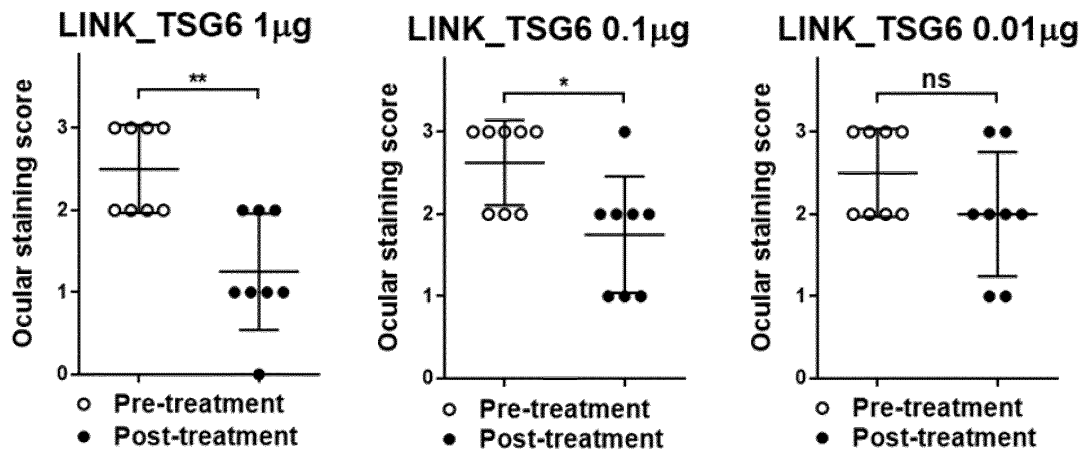


Figure 3A

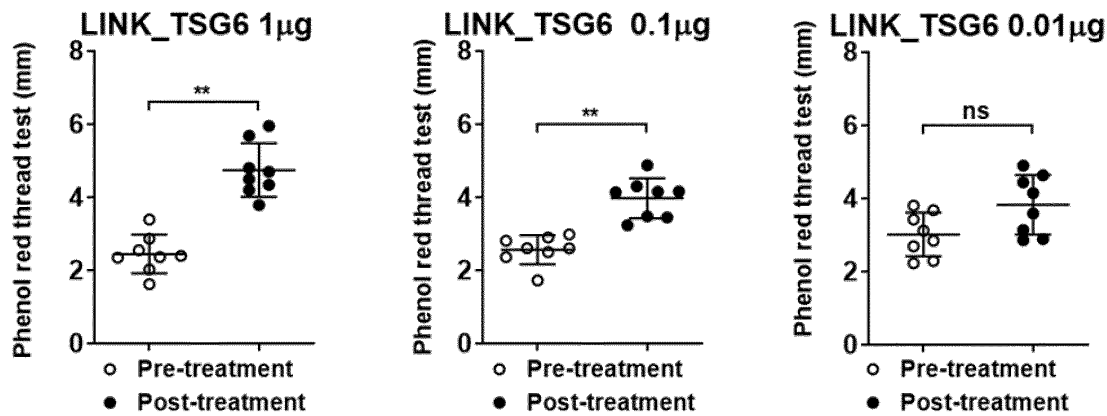


Figure 3B

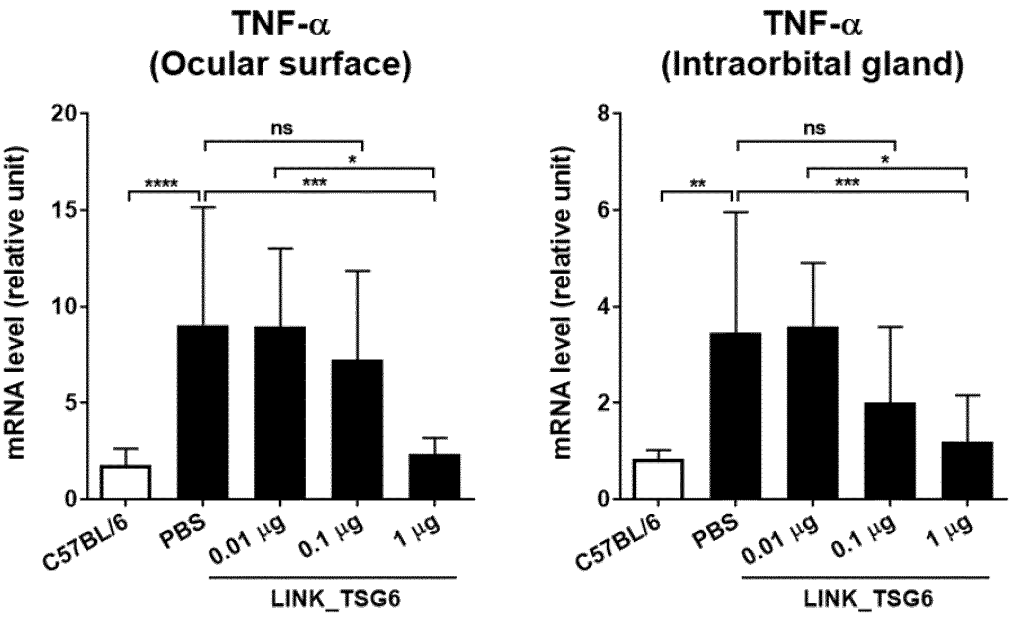


Figure 3C

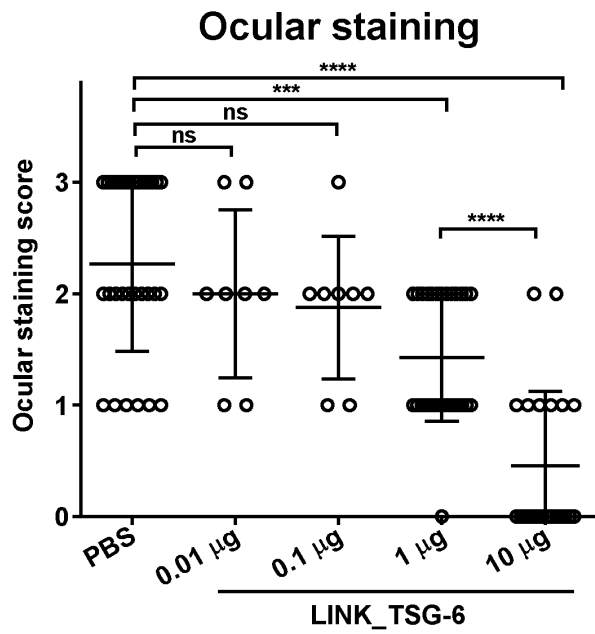


Figure 4A

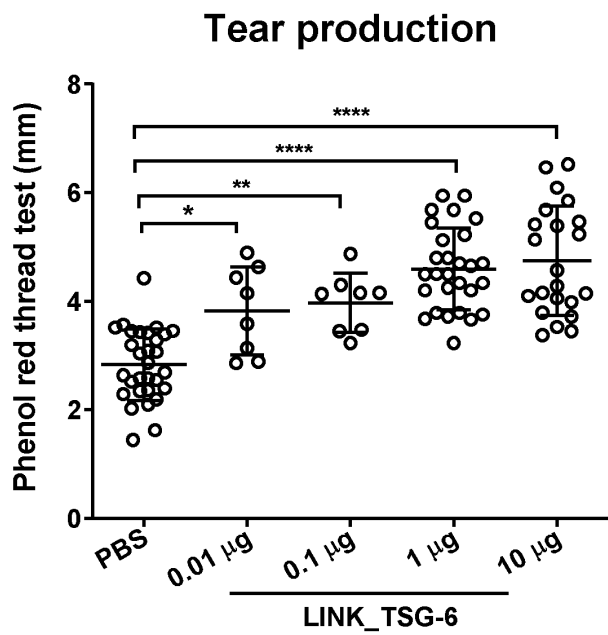


Figure 4B

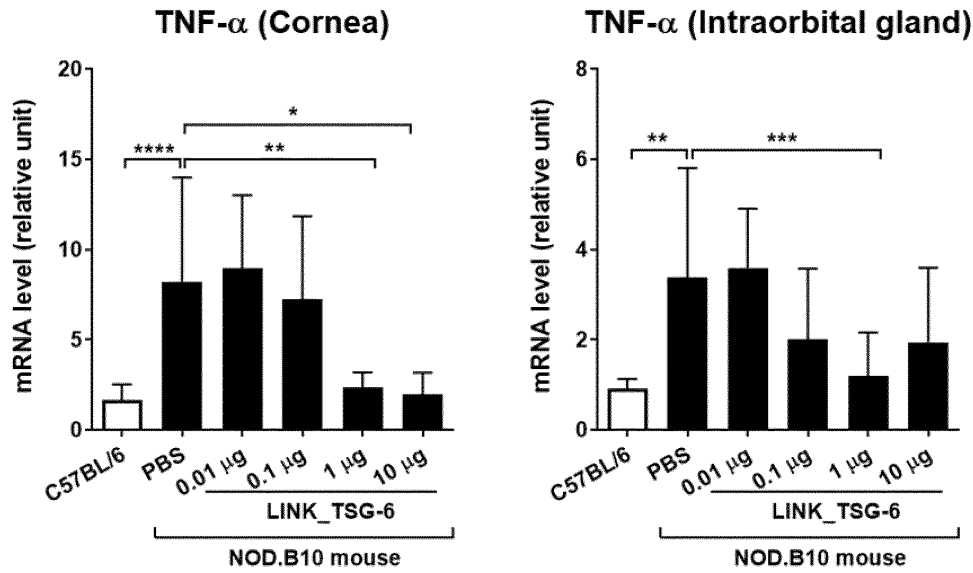


Figure 4C

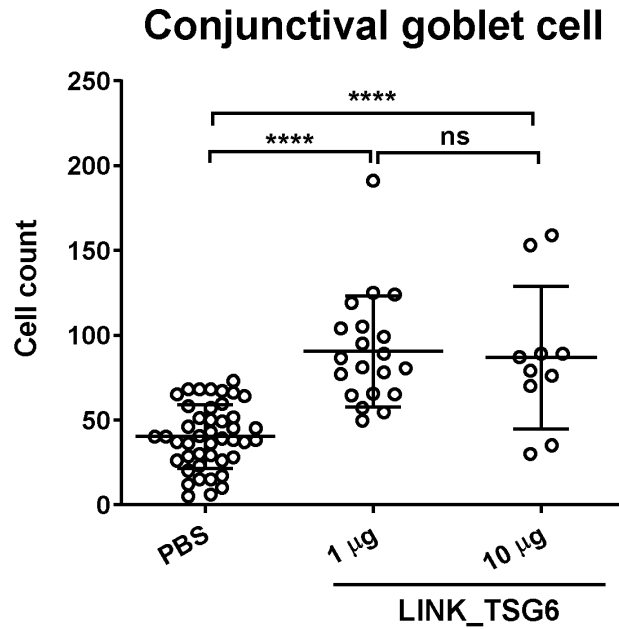


Figure 4D

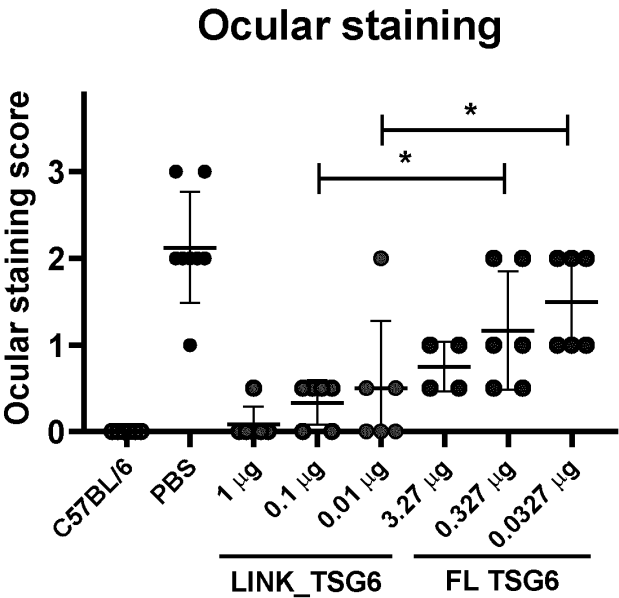


Figure 5A

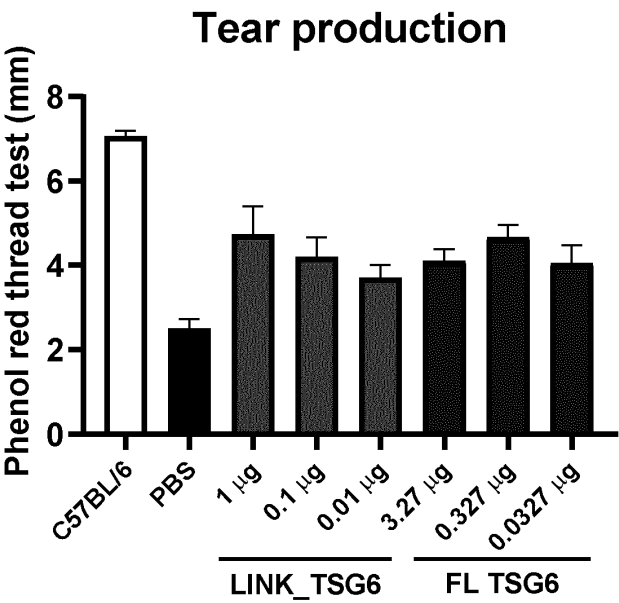


Figure 5B

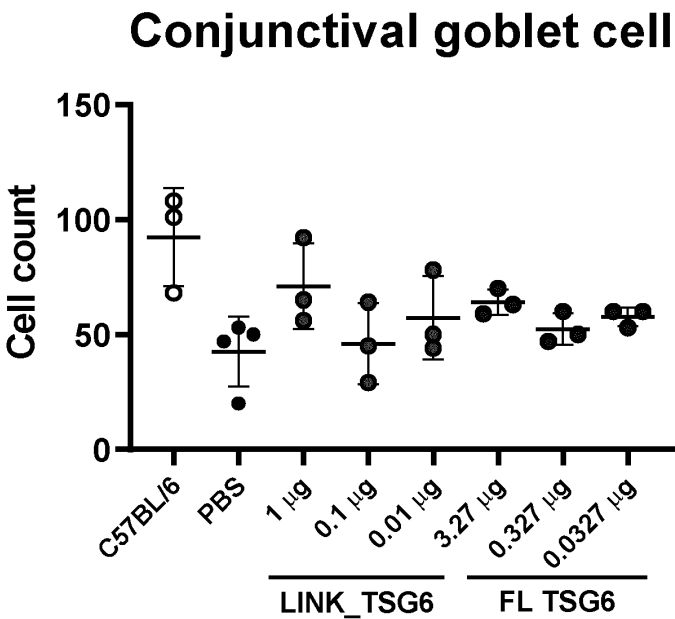


Figure 5C

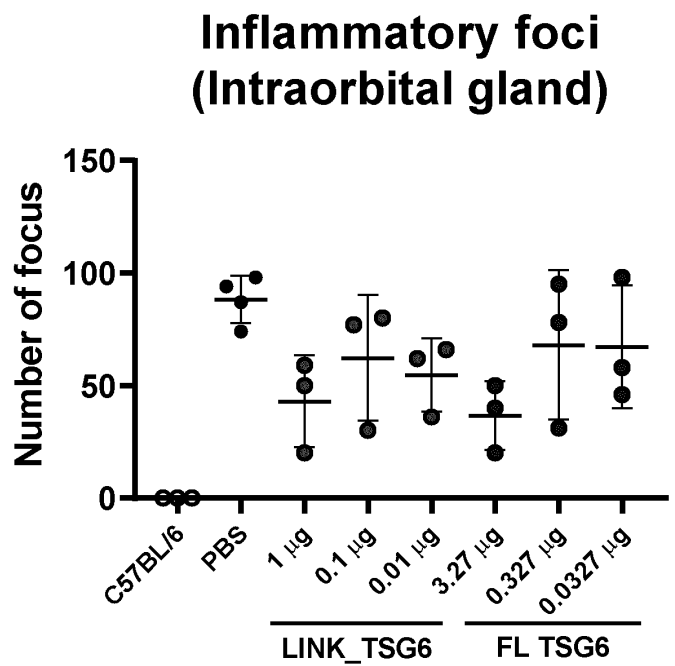


Figure 5D

Pre-treatment

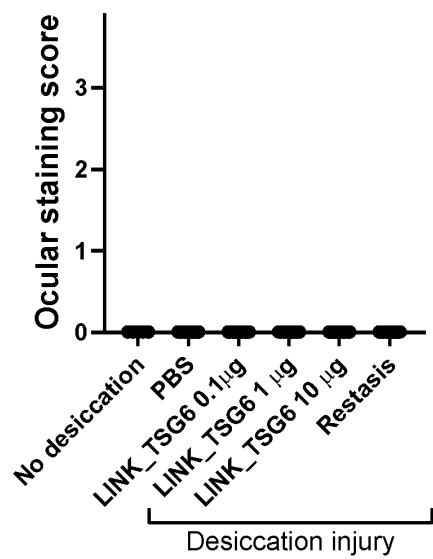


Figure 6A

Post-treatment

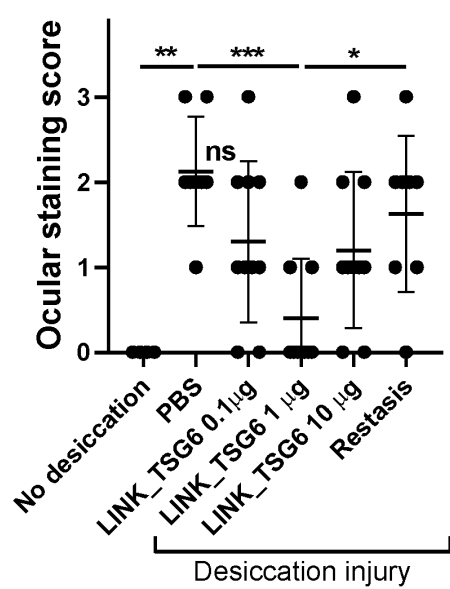


Figure 6B

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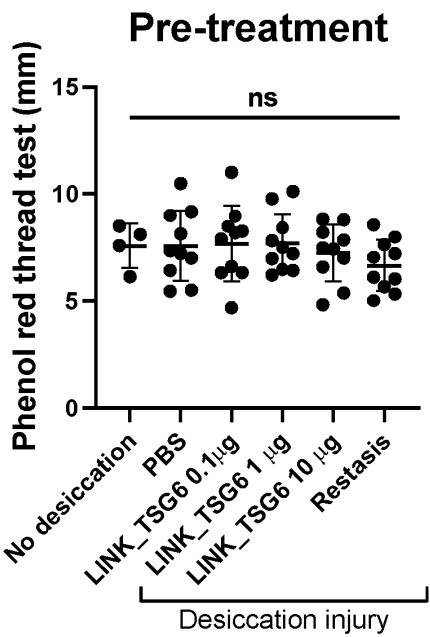


Figure 6C

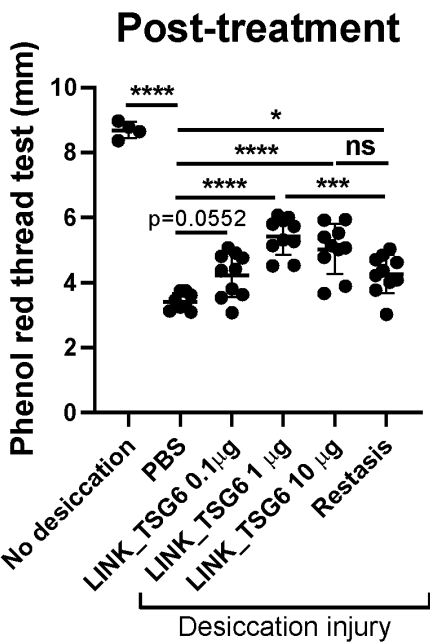


Figure 6D

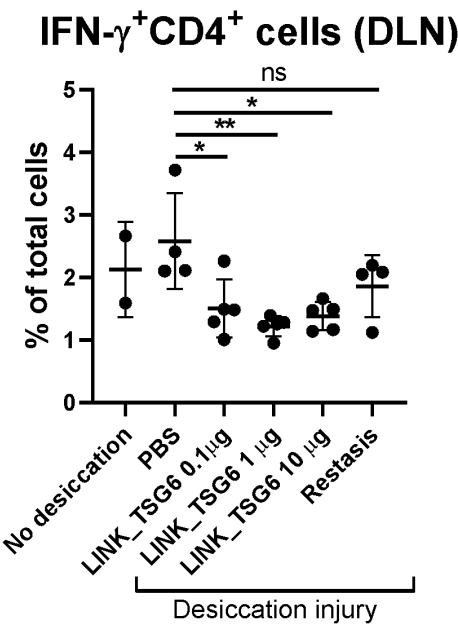


Figure 6E

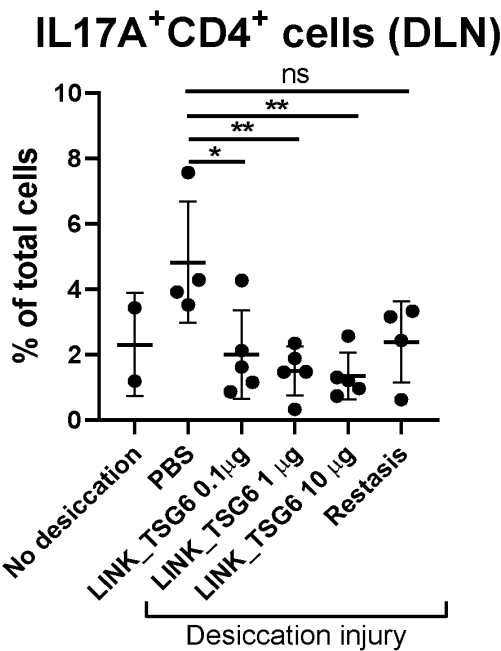


Figure 6F

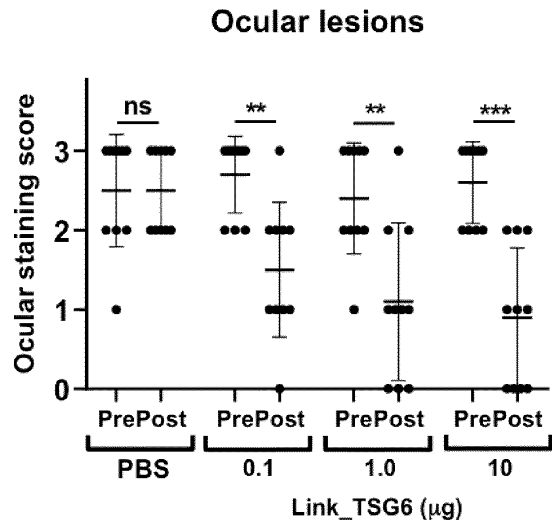


Figure 7A

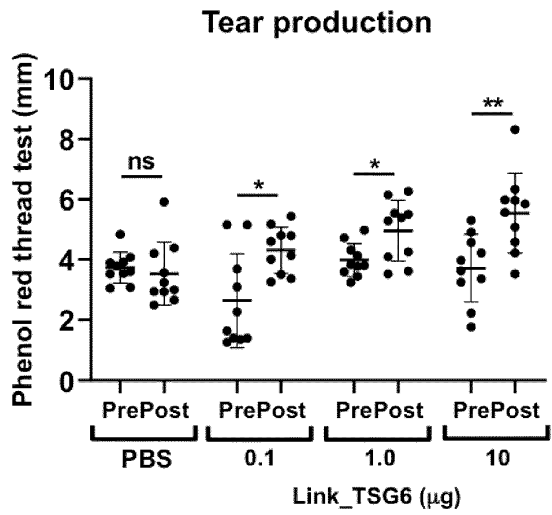


Figure 7B

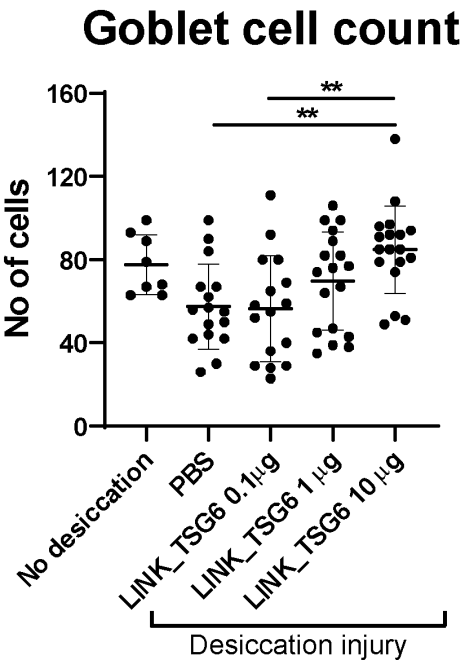


Figure 7C

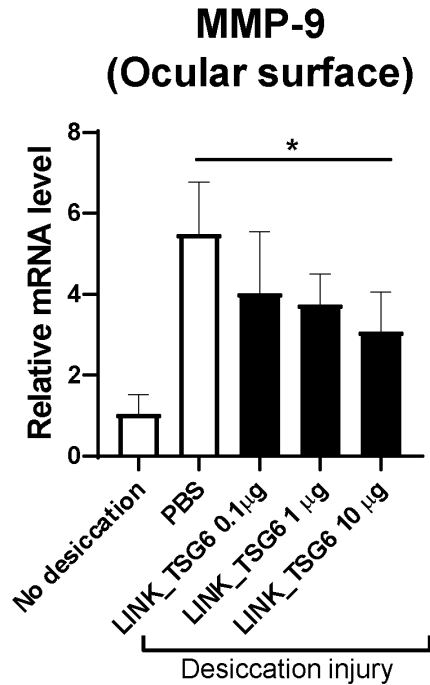


Figure 7D

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Pre-treatment

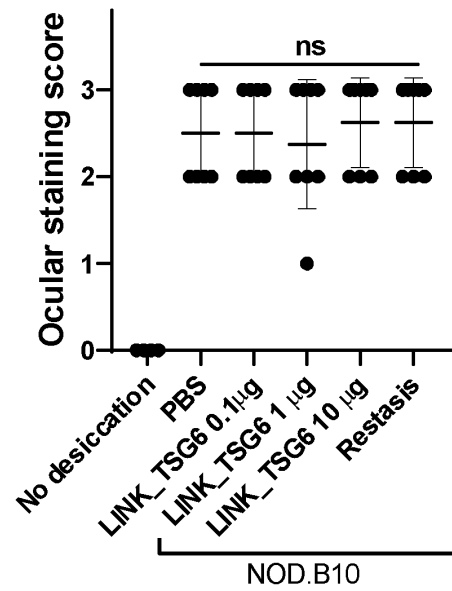


Figure 8A

Post-treatment

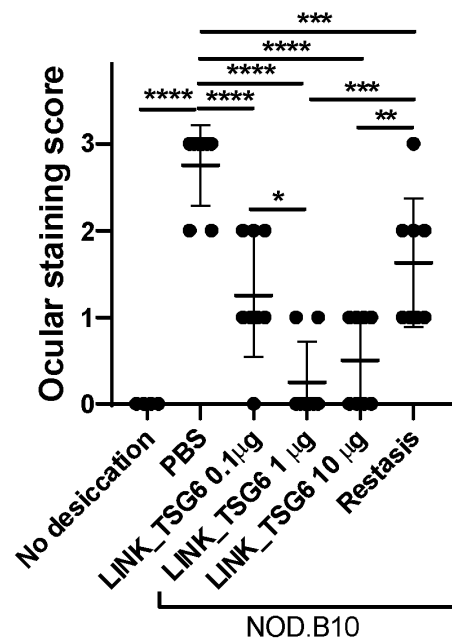


Figure 8B

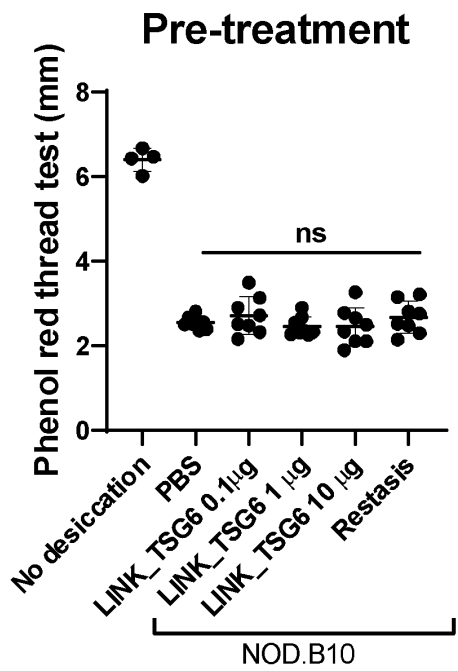


Figure 8C

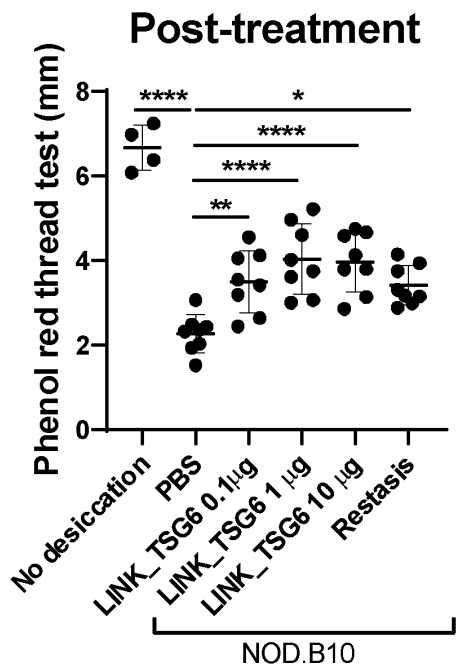


Figure 8D

Conjunctival goblet cells

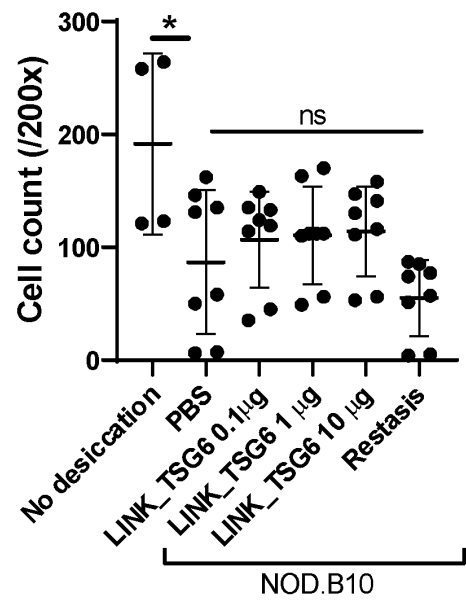


Figure 8E

Intraorbital gland
CD3⁺ inflammatory foci

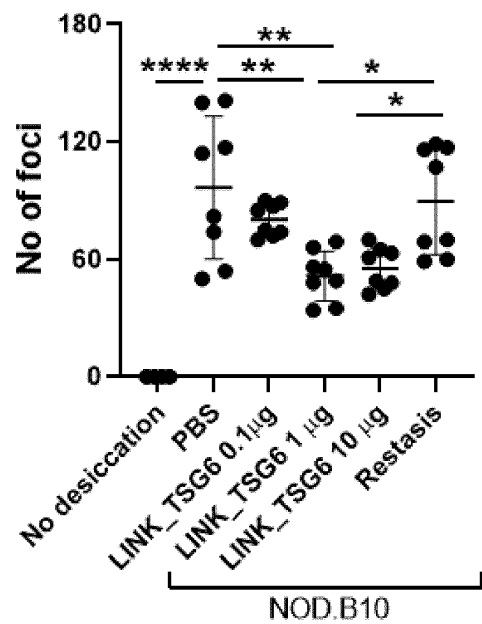


Figure 8F